IN THE SPECIFICATION

Please replace the paragraph beginning on page 9, line 11 with the following replacement paragraph:

The term "best alignment" or "optimal alignment" is intended to denote the alignment for which the percentage identity determined as described hereinafter is the highest. Comparisons between two nucleotide or amino acid sequences are conventionally carried out: by comparing these sequences after having optimally aligned them, said comparison being carried out by segment or by "window of comparison" so as to identify and compare local regions of sequence similarity. The optimal alignment of the sequences for the comparison can be carried out in particular using one of the following algorithms: the local homology algorithm of Smith and Waterman (1981), the local homology algorithm of Neddleman and Wunsch (1970), the similarity search method of Pearson and Lipman (1988), the computer programs using these algorithms (GAP, BESTFIT, BLAST P, BLAST N, BLASTX, TBLASTX, FASTA and TFASTA in the Wisconsin Genetics Software Package (Genetics Computer Group, 575 Science Dr., Madison, WI) or on internet servers, in particular those of the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov) (hypertext transfer protocol available on the worldwide web at ncbi.nlm.nih.gov), of the EMBL (http://www.embl.org) (hypertext transfer protocol available on the worldwide web at embl.org) and of the Ensembl project (http://www.ensembl.org) (hypertext transfer protocol available on the worldwide web at ensembl.org)).

Please replace the paragraph beginning on line 21 of page 34 with the following replacement paragraph:

The analysis of the primary sequence of ZnT-8 and the prediction of the transmembrane domains were carried out with the TMpred (http://www.ch.embnet.org/

~~software/TMPRED_form.html)~~ <u>(hypertext transfer protocol on the worldwide web at</u>

<u>ch.embnet.org/software/TMPRED_form.html) and SOSUI</u>

~~(http://sosui.proteome.bio.tuat.ac.jp/sosuimenu0.html)~~ <u>(hypertext transfer protocol on the</u>

<u>worldwide web at sosui.proteome.bio.tuat.ac.jp.sosuimenu).html) programs.</u>